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Authors

Cummins, Breschine

Johnson, Kara

Schneider, John A

et al.

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Leveraging social networks for identification of people with HIV who are virally unsuppressed

Breschine Cummins[a], Kara Johnson[a], John A. Schneider[b,c], Natascha Del Vecchio[c], Niema Moshiri[d], Joel O. Wertheim[e], Ravi Goyal[e,*] and Britt Skaathun[e,*]

Objectives: This study investigates primary peer-referral engagement (PRE) strategies to assess which strategy results in engaging higher numbers of people with HIV (PWH) who are virally unsuppressed.

Design: We develop a modeling study that simulates an HIV epidemic (transmission, disease progression, and viral evolution) over 6 years using an agent-based model followed by simulating PRE strategies. We investigate two PRE strategies where referrals are based on social network strategies (SNS) or sexual partner contact tracing (SPCT).

Methods: We parameterize, calibrate, and validate our study using data from Chicago on Black sexual minority men to assess these strategies for a population with high incidence and prevalence of HIV. For each strategy, we calculate the number of PWH recruited who are undiagnosed or out-of-care (OoC) and the number of direct or indirect transmissions.

Results: SNS and SPCT identified 256.5 [95% confidence interval (CI) 234–279] and 15 (95% CI 7–27) PWH, respectively. Of these, SNS identified 159 (95% CI 142–177) PWH OoC and 32 (95% CI 21–43) PWH undiagnosed compared with 9 (95% CI 3–18) and 2 (95% CI 0–5) for SPCT. SNS identified 15.5 (95% CI 6–25) and 7.5 (95% CI 2–11) indirect and direct transmission pairs, whereas SPCT identified 6 (95% CI 0–8) and 5 (95% CI 0–8), respectively.

Conclusion: With no testing constraints, SNS is the more effective strategy to identify undiagnosed and OoC PWH. Neither strategy is successful at identifying sufficient indirect or direct transmission pairs to investigate transmission networks.

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Keywords: contact tracing, engagement, HIV, people with HIV, recruitment, social networks

Introduction

In 2019, the US Health and Human Services established the Ending the HIV Epidemic (EHE) initiative to eliminate new HIV infections by 2030 [1]. The EHE initiative outlines four strategies, all of which require rapidly engaging individuals in HIV services through diagnosing people early, link-to-care, or re-engagement for individuals out-of-care (OoC). Engagement is challenging and will increase in difficulty as the epidemic becomes more concentrated among those who are historically disenfranchised, such as Black sexual minority men (BSMM) [2–4]. Prioritizing the BSMM population is critical to achieving EHE goals as approximately a quarter of all new HIV infections in the United States are among BSMM [5], and BSMM are less likely to be virally

[a]Department of Mathematical Sciences, Montana State University, Bozeman, MT, [b]Department of Medicine, University of Chicago, [c]Department of Public Health Sciences, University of Chicago, Chicago, IL, [d]Computer Science and Engineering Department, and [e]Division of Infectious Diseases and Global Public Health, Department of Medicine, University of California, San Diego, La Jolla, CA, USA.

Correspondence to Britt Skaathun, PhD, MPH, 9500 Gilman Drive, Mail Code 0507, La Jolla, CA 92093-0507, USA.

Tel: +1 619 543 5011; e-mail: bskaathun@health.ucsd.edu.

* R.G. and B.S. are joint senior authors.

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suppressed [6]. Engagement in care among this group is low as a result of stigma experienced in healthcare settings, lack of insurance, unstable housing, and psychological factors [7–9]. However, engagement is critical in the United States; it is estimated that 13–15% of people with HIV (PWH) are currently undiagnosed and that another 37% are OoC [10]. This has serious consequences as unaware and OoC PWH are estimated to account for 80% of transmissions [11].

There have been several efforts to engage individuals. For example, the standard of care employed by Public Health Departments across the United States for identifying individuals who are unaware of their HIV infection is contact tracing (i.e. partner services) [12,13]. This process involves eliciting names of sexual and drug use contacts from people newly diagnosed with HIV and inviting them to get tested for HIV [12,13]. This approach has not been widely effective, producing a low number of contacts of newly HIV diagnosed clients. In a review of 51 public health jurisdictions, only 0.9 contacts were identified per newly HIV diagnosed 'index' [14]. Per recommendation by the Centers for Disease Control and Prevention (CDC), the focus of partner services is on PWH who are newly diagnosed rather than re-engaging PWH who are OoC [15]. However, new evidence shows that focusing partner services on contacts of previously diagnosed PWH is also effective at engaging and re-engaging PWH [16]. The objective of this manuscript is to explore the effectiveness of peer recruitment strategies for engagement and re-engagement among BSMM, where we define recruitment as the acceptance of a peer invitation and HIV testing.

Although the ultimate goal for engaging/re-engaging people who are undiagnosed and/or OoC is to reduce HIV transmission, it is unclear what recruitment strategy can most effectively identify PWH who have high HIV transmission potential (i.e. PWH who are virally unsuppressed), and what strategy enables a better characterization of the underlying HIV transmission network. A contributing factor to the low identification rate is that at-risk populations often do not trust the medical community [3], or are more likely face stigma from partners if referred, and partners may face stigma being named by someone living with HIV/STIs. Interventions that recruit social contacts, either in addition to or in place of risk contacts, have been more effective at locating those with undiagnosed HIV infection, in part because people tend to obtain and transmit information primarily through informal social networks, especially their friends [3,17]. In addition, naming a friend, or family member rather than a sex partner also decreases stigma [18–20]. This 'social network strategy' (SNS) is promoted by the CDC, with studies showing that up to 6% of people tested using SNS are unaware of their HIV infection [5,21–23].

We investigate two primary Peer-Referral Engagement strategies (PRE strategies) for identifying PWH who are undiagnosed, PWH who are OoC, PWH pairs who have similar HIV genetic sequences (i.e. indirect HIV transmission pairs), and PWH pairs where HIV transmission occurred. We investigate one PRE strategy with recruitment based on social partners and another based on sexual partners. We simulate PRE strategies for BSMM in Chicago, which is located within an EHE jurisdiction [1].

Methods

Overview

To evaluate PRE strategies, it is necessary to have realistic social and sexual contact networks, as well as knowledge about HIV transmissions that occur within this population (the transmission network). However, complete social, sexual, and transmission networks are generally unknown. To evaluate PRE strategies, we conducted a robust simulation study with three modeling components on simulated networks (see Fig. 1a).

We first generated social and sexual networks that represented connections among BSMM in Chicago. We used a congruence class model (CCM) [24] to generate sample networks. Secondly, we simulated HIV spread among BSMM using an epidemic transmission model called FAVITES (FrAmework for Viral Transmission and Evolution Simulation) [25]. FAVITES produces a transmission network and simulated genetic sequence data. Together, components 1 and 2 generate necessary data to model and assess the PRE strategies (component 3). Fig. 1a outlines these components, including model assessment on key outcomes.

Data

The first and third components were parameterized using data from a longitudinal study of BSMM ages 16–29 who reside in Chicago; details of the study, including sampling, recruitment, and data collection, have been previously described [26–28]. The cohort was obtained using respondent-driven sampling to recruit 618 young BSMM. Respondents were evaluated at baseline, 9, and 18 months beginning June 2013. Each participant answered a set of name-generating questions at each study visit on their social and sexual networks. Participants were asked to list up to five confidants with whom they 'discuss things that are important to you' along with demographic information, such as name, gender (male, female, transgender), age, education, employment status, ethnicity (Hispanic or not), and race. Participants were also asked to list their (up to) five most recent sexual partners in the past 6 months. The degree distribution of sexual partners, D^{cn}, was estimated from these data (Supplemental Table S1, http://links.lww.com/QAD/D23). Study participants were asked how many SMM they know, and these survey responses together with named confidants permitted an estimate of the distribution of

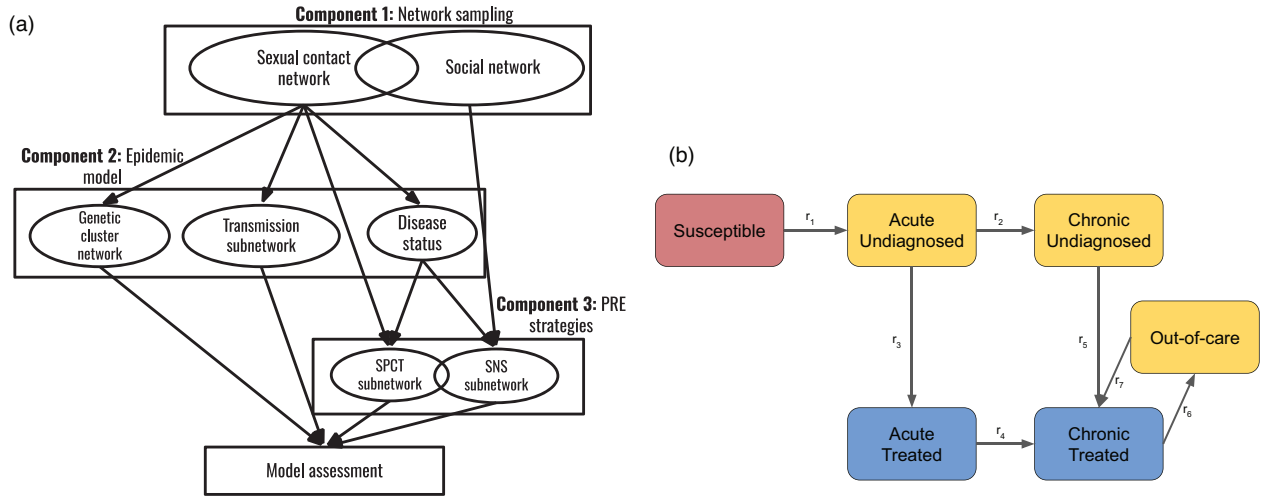


Fig. 1. Simulation framework. (a) First a contact network is sampled, and then a social network is sampled with a specified overlap with the contact network (component 1). An epidemic model is run on the contact network for a simulated time period of 6 years (component 2). The outputs of the epidemic model are viral molecular sequences that can be transformed into a genetic cluster network; a collection of transmission events defining a transmission network; and the disease status of each individual in the simulation. Finally, SPCT is simulated on the sexual contact network, and SNS is simulated on the social network (component 3). The disease status and transmission relationships of the sampled individuals are then compared. (b) Division of risk population into disease status categories (compartments). Our epidemiological model consists of six disease states. Colors indicate treatment status. Pink denotes susceptible individuals, yellow compartments show individuals not presently under treatment (i.e. undiagnosed/treatment-naive, or out-of-care), and blue compartments indicate individuals currently under treatment. Individuals in the susceptible population become infected and transition to the acute undiagnosed state at rate r_1. From the acute undiagnosed state, individuals either remain untreated and transition to chronic undiagnosed at a rate of r_2 or initiate treatment and transition to acute treated at a rate r_3. Individuals in the acute treated and chronic undiagnosed compartments enter a chronic treated state with transition rates r_4 and r_5, respectively. The out-of-care compartment contains individuals that are currently not treated but have been in the past. The out-of-care and chronic treated compartments may mutually transition with rates of r_6 and r_7.

BSMM social contacts, D^{sn} (Supplemental Table S2, http://links.lww.com/QAD/D23).

Simulation components

Component 1: generating sexual and social networks

We estimated the population size of the BSMM in Chicago to be 15 397 (see Supplement, http://links.lww.com/QAD/D23). Each of the 15 397 nodes in the sexual contact network, g^{cn}, represents an individual, while each edge represents a sexual relationship between two BSMM. Our sexual networks are generated using a CCM, which is defined by a network property or set of properties and a probability mass function on the congruence classes defined by values of the network property. An important network property to model epidemic spread is the distribution of the number of sexual partners, which is referred to as a degree distribution, denoted D^{cn}. For simulated sexual contact networks, we model degree distributions based on data from uConnect [27,29] (see Supplemental Table S1, http://links.lww.com/QAD/D23), assuming that the degree distribution follows a multinomial distribution based on D^{cn} parameterized by maximum likelihood estimates.

We generate a social network, g^{sn}, using a two-step process. The first consists of generating an initial network, $g^{sn}_{initial}$, using a CCM with a multinomial distribution on the degree distribution that is parameterized from the social partner data from the uConnect cohort using maximum likelihood estimates. The uConnect study allowed participants to name SMM social contacts irrespective of race, that is, not restricted to BSMM [27,29]. Based on demographic data provided by respondents, 97% of SMM social partners were BSMM. Therefore, we assume that the degree distribution of social contacts in the sexual minority men community approximates the degree distribution of the BSMM community, D^{sn} (Supplemental Table S2, http://links.lww.com/QAD/D23). Secondly, we randomly selected 13% of g^{cn} edges and added this subgraph to $g^{sn}_{initial}$ to generate g^{sn} (the percentage of sexual partner pairs in the BSMM population that were also in the social network was 13% in the uConnect study). This addition is a necessary step since g^{cn} and $g^{sn}_{initial}$ are generated independently.

Component 2: simulating HIV epidemic, transmission network, and molecular sequences

We simulated an HIV epidemic process using FAVITES, which ingests a sexual network, simulates an epidemic process, and outputs a transmission network g^{tn} and associated HIV sequence data. FAVITES uses an epidemic compartmental model customized to HIV to simulate disease transmission. Our epidemic model divided the BSMM population into six compartments: susceptible,

undiagnosed acute, treated acute, undiagnosed chronic, treated chronic, and OoC; see Fig. 1b. Susceptible individuals are uninfected; individuals that have acute or chronic treated infections are PWH undergoing antiretroviral therapy (ART), while PWH without a diagnosis and OoC individuals (all assumed to have a diagnosis) are not on ART. See Supplement for initial population sizes in each compartment, http://links.lww.com/QAD/D23.

PWH have a probability of transmitting HIV to each of their susceptible sexual partners. The probabilities for transmission from individuals with treated acute, undiagnosed acute, and undiagnosed chronic infections were from published literature (Supplemental Table S3 and Supplemental Figure S1, http://links.lww.com/QAD/D23) [25]; PWH in the chronic treated compartment were assumed to have a zero transmission rate. The transmission rate from OoC individuals to susceptible individuals was calibrated to ensure an incidence rate of approximately 1.4% (see Supplemental Figure S2, http://links.lww.com/QAD/D23); this incidence was derived by applying data from the Enhanced HIV/AIDS Reporting System (eHARS) in Chicago to the estimate of the BSMM population size in 2019 [30].

Compartment transmissions are Poisson processes. Individuals transitioned from acute to chronic disease status with a mean of approximately 6 weeks [31], regardless of treatment state. The mean transition time from acute undiagnosed to acute treated was 1 year [25], and chronic undiagnosed to chronic treated was approximately 3.3 years (see Supplement, http://links.lww.com/QAD/D23). PWH may transition back and forth between the chronic treated and OoC compartments. The mean transition time from OoC to chronic treated (re-engagement) was 5.9 years [32] and chronic treated to OoC was then calibrated to 1.8 years in order to ensure that there were not multiple transitions between these compartments within a 12-month period (see Supplement, http://links.lww.com/QAD/D23), which is not consistent with the standard definition of OoC [33].

Epidemics were simulated over a 6-year period, without a specific starting year (late teens are reasonable), providing each individual's disease status, all transmission events, and all viral sequences. Sequencing occurred at the end of the simulation. The evolutionary model and associated parameters are those used in previous studies with FAVITES [25,34] (Supplemental Table S3, http://links.lww.com/QAD/D23). FAVITES does not currently model PRE strategies coincident with an epidemic, so the simulated disease spread was performed first to provide a reasonable estimate of a population in the midst of an epidemic.

Component 3: simulating peer-referral engagement strategies

We simulated two PRE strategies at the end of the epidemic simulation before further significant transmission occurred. The first strategy modeled recruitment of social partners (SNS for social network strategy) and the second modeled recruitment of sexual partners through peer-referral contact tracing (SPCT). To simulate SNS, we conducted respondent-driven sampling on g^{sn}, whereas SPCT uses g^{cn}. Both PRE strategies start with an initial group of PWH respondents (seeds), who then recruit others. In respondent-driven sampling, each individual attempts to recruit a fixed number of their social contacts for participation by providing them with a voucher; these contacts accept and participate with probability p^{sns}. The new recruits continue this process until a specified sample size is reached. In SPCT, the PWH seed attempts to recruit all sexual partners; a partner accepts with a fixed probability p^{ct}. Only PWH continue recruiting in the SPCT strategy. The process continues until none of the recruits are PWH; unlike SNS, SPCT does not have a fixed sample size.

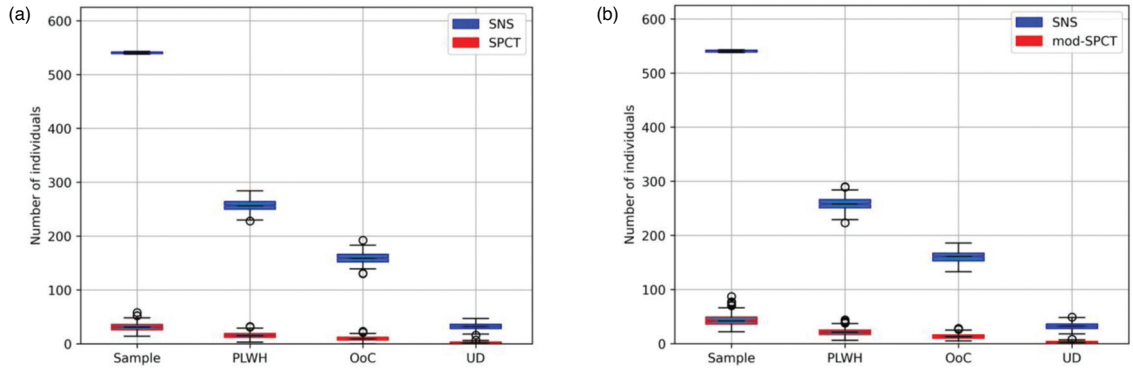
The number of vouchers distributed per individual (6) in SNS, the initial population of seed individuals (62) in both SNS and SPCT, and the target sample size for SNS (600) were taken from the uConnect study design. The probability $p^{sns} = 39.4\%$ was estimated from uConnect outcomes by taking the proportion of vouchers returned from individuals who reported a single social contact. Although the uConnect data recruitment strategy specified only young BSMM, we use the acceptance rate for our simulations to represent recruitment of the entire BSMM population in Chicago (we later relaxed this assumption). The probability p^{ct} was estimated from the literature to be 17.5% [35] (Supplemental Table S4, http://links.lww.com/QAD/D23).

Model assessment of peer-referral engagement strategies

The measure of success of a PRE strategy used in this article was the total number and proportion of PWH recruited during SNS or SPCT and stratified by those OoC or undiagnosed. We also assessed the number of pairs of individuals with direct or indirect transmission events that were sampled in each recruitment strategy. To assess possible indirect transmissions, we computed genetic distances between the HIV sequence data simulated by FAVITES using the TN93 nucleotide substitution model [36–38]. Putative linkage in a molecular network g^{gcn} is inferred when the genetic distance between two sequences is below 1.5% sequence divergence.

Sensitivity analyses

We conducted three sensitivity analyses. The first was a modified version of SPCT (mod-SPCT) where all individuals (not just PWH) were asked to continue recruiting all sexual partners until no further individuals chose to participate, assuming the same probability of recruitment. The motivation for mod-SPCT was to exclude the possibility that only following up with PWH was the cause of small sample sizes in SPCT (Fig. 2a). The second analysis increased p^{ct} from 17 to 27% and decreased p^{sns} from 40 to 30% to assess the impact of uncertainty in



(c)

Subpopulation	SNS percentage of sample median with 95% C.I. (2 independent simulations)	SPCT percentage of sample median	mod-SPCT percentage of sample median
PLWH	47.5% (43.3%, 51.6%) 47.7% (44.1%, 51.7%)	50.0% (31.8%, 68.0%)	50.0% (35.3%, 68.6%)
OoC	29.4% (26.3%, 32.9%) 29.7% (26.2%, 33.6%)	30.8% (15.6%, 50.0%)	31.0% (19.7%, 47.7%)
Undiagnosed (UD)	5.9% (3.9%, 7.9%) 5.9% (4.1%, 8.1%)	6.5% (0.0%, 15.6%)	6.1% (0.0%, 15.2%)

Fig. 2. (a) Comparison of number of recruited people with HIV between social network strategies and sexual partner contact tracing. The panel shows the number of individuals recruited from SNS and SPCT in total, the subsample of these that are PWH, the further subsample that are out-of-care, and lastly the subsample of PWH that are undiagnosed. The boxplots show the distribution of the median individuals over 250 simulations, 25 and 75% quartiles, whiskers out to 1.5 times the interquartile distance, and outliers beyond. The label 'Sample' refers to the total sample size excluding seed individuals. PWH indicates infected individuals that were sampled, regardless of diagnosis or treatment state. OoC indicates the sampled individuals in the OoC compartment. 'UD' refers to people who are undiagnosed that were sampled, whether in the acute or chronic phase of the disease. Medians and confidence intervals are given in Supplemental Table S5, http://links.lww.com/QAD/D23. (b) Comparison of number of samples of PWH between SNS and mod-SPCT, where both infected and uninfected individuals are asked to recruit sexual partners. The SNS strategy remained unchanged as expected, except for slight differences because of stochasticity. The mod-SPCT strategy yielded only slightly better numbers than SPCT in panel (a), with a median sample size of 42 (95% CI 24–65). Other medians and CIs are given in Supplemental Table S6, http://links.lww.com/QAD/D23. (c) Comparison of percentage of recruited subpopulation with respect to sample size for SNS, SPCT, and mod-SPCT. The percentages of the PWH groups were computed as a proportion of sample size. For example, PWH recruited via SNS is 47.5% (95% CI 43.3–51.6%) of the SNS sample size (median 540, 95% CI 538–543), while PWH sampled via SPCT is 50% (95% CI 31.8–68%) of the SPCT sample size (median 31, 95% CI 18–46). Other percentages with 95% CIs are shown in the table with the corresponding sample medians/CIs in Supplemental Table S5, http://links.lww.com/QAD/D23. The first column indicates the subpopulation for which percentages are reported; the second column shows results for SNS (blue boxes) in both panels (a) and (b); the third column reports percentages for SPCT in panel (a) (red boxes); and the fourth column reports percentages for mod-SPCT in panel (b) (red boxes). While the absolute sample sizes between SNS and SPCT/mod-SPCT are very different [compare blue and red boxes in panels (a) and (b)], the percentage of PWH subpopulations recruited is very similar between PRE strategies. SNS, social network strategies; SPCT, sexual partner contact tracing.

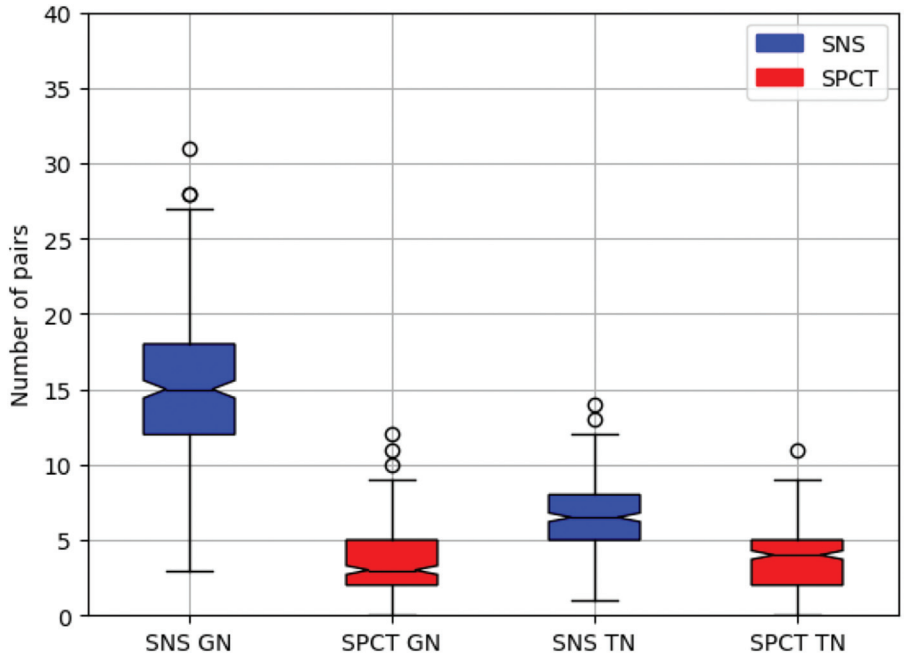


Fig. 3. Comparison of number of pairs of individuals with genetically similar viral sequences (GN) and direct transmission events (TN) between social network strategies and sexual partner contact tracing. The boxplots show the distribution of the median individuals over 250 simulations, 25 and 75% quartiles, whiskers out to 1.5 times the interquartile distance, and outliers beyond. The number of pairs was less than 35 in all cases. In comparison, the number of pairs in each of the genetic cluster and transmission networks numbered in the thousands. Medians and CIs in Supplemental Table S7, http://links.lww.com/QAD/D23. CI, confidence interval.

acceptance rates. The third analysis varied the initial prevalence of HIV among BSMM (36.3%, see Supplement, http://links.lww.com/QAD/D23) to 27.2, 18.1, and 9.1%, representing HIV prevalences of 75, 50, and 25% of baseline.

Results

Results for number of people with HIV recruited

We performed 250 independent simulations and compared outcomes from SNS and SPCT. We found that overall SNS outperformed SPCT on total number of PWH recruited as well as stratified by those OoC and undiagnosed. The median identification of PWH by SNS was 256.5 (95% CI 234–279) compared with 15 (95% CI 7–27) by SPCT. For PWH in the OoC and undiagnosed populations, SNS identifies 159 (95% CI 142–177) and 32 (95% CI 21–43), respectively, compared with 9 (95% CI 3–18) and 2 (95% CI 0–5] by SPCT; see Fig. 2a. The difference in absolute numbers between the strategies is because of the larger number of recruits under SNS compared with SPCT. In terms of percentages, the two strategies are nearly identical; see Fig. 2c.

Results for direct and indirect HIV transmission pairs

PRE strategies were assessed on the number of direct/indirect HIV transmission pairs identified. A direct transmission pair occurred if both PWH were connected by an edge in g^{tn}, whereas an indirect pair was represented by an edge in g^{gcn}. For both PRE strategies, an insignificant number of direct and indirect pairs were found (Fig. 3). We conclude that both SNS and SPCT are inefficient at recovering direct and indirect HIV transmission pairs at the sample sizes explored here. This conclusion holds when viral sequencing occurs at the moment of infection (Supplemental Figure S3, http://links.lww.com/QAD/D23).

Results from sensitivity analyses

In the first analysis (mod-SPCT), we saw slight, but not substantial, improvement in sample sizes (Fig. 2 and Supplemental Tables S5 and S6, http://links.lww.com/QAD/D23), indicating that continuing recruitment with all sexual partners does not significantly increase the proportion of PWH recruited.

For the second analysis (variance of acceptance rate), the sample size for SPCT increased moderately with increasing acceptance rate (Fig. 4a, Supplemental Table S8, http://links.lww.com/QAD/D23). In contrast, decreasing the acceptance rate for SNS from 40 to 30% caused no change in the sample size of recruited individuals (medians and CIs in Supplemental Table S9, http://links.lww.com/QAD/D23). Furthermore, the decrease in rate did not affect the number of PWH recruited with SNS (Fig. 4b). We conclude that the higher degree distribution of the social

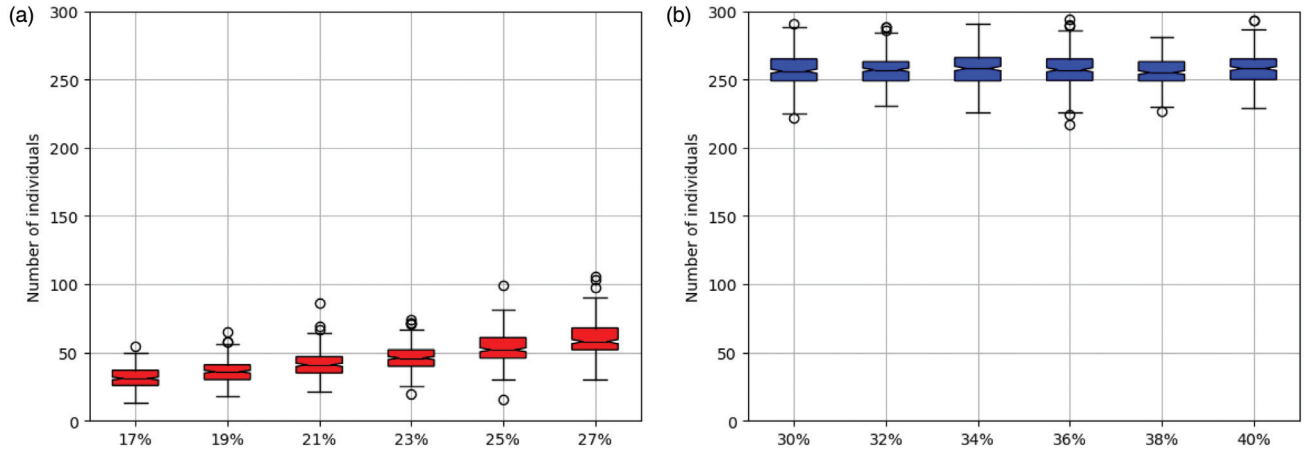


Fig. 4. Yield as a function of acceptance rate. (a) Total sample size attained for SPCT at acceptance rates of 17–27%. (b) Number of PWH recruited under SNS [the total sample size was 602 (95% CI 600–605)] for acceptance rates from 30 to 40%. Medians and CIs in Supplemental Tables S8–S9, http://links.lww.com/QAD/D23. SNS, social network strategies; SPCT, sexual partner contact tracing.

network is responsible for the larger sample sizes, not the acceptance rate. Similarly, the lower degree distribution in the SPCT network is likely the primary cause of the low sample size.

In the third analysis (variance of HIV prevalence), the number of new PWH recruited drops as prevalence decreases (Fig. 5). The drop is more pronounced in SNS compared with SPCT. At our estimated prevalence of 36.3%, the proportions of PWH, OoC PWH, and undiagnosed PWH are similar between the two strategies. At less than 18.1% prevalence, SPCT shows a noticeable advantage in the proportion of all, OoC, and undiagnosed PWH identified. This corresponds to fewer administered HIV tests per recruitment. In all cases, SNS returns a greater absolute number of individuals because of its greater sample size but its proportional results are only comparable to SPCT at the highest prevalence.

Discussion

We examined the relative performance of two PRE strategies, social network-based (SNS) and sexual network-based (SPCT), in identifying subpopulations of PWH at high risk of transmitting HIV. Our simulation results indicate that SNS identifies a greater number of PWH who are undiagnosed and OoC compared with SPCT. However, the two strategies produce equal proportions of these outcomes, consistent with nearly equal proportions of newly diagnosed BSMM from both social and sexual PRE strategies in Baytop *et al.* [39]. This suggests that a larger proportion of the total population of PWH can be identified by using a SNS strategy, with the number of administered tests proportionately the same for each newly diagnosed individual as in contact tracing for high HIV prevalence. For low prevalence, if the number of tests is a concern, then contact tracing may be

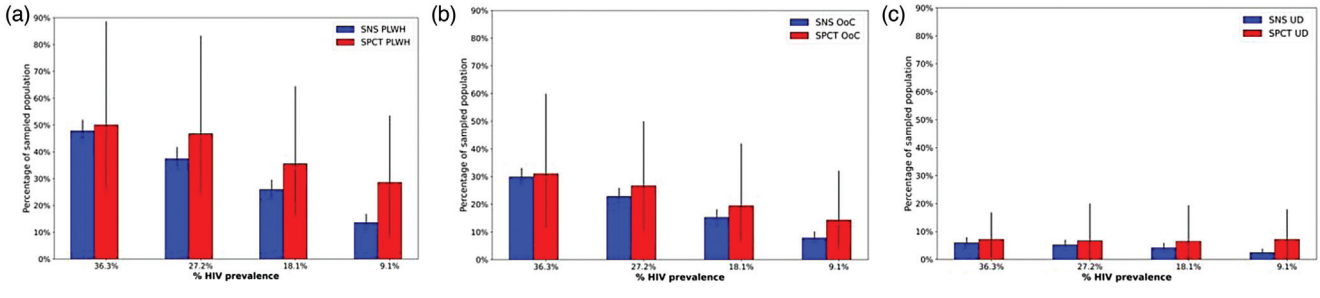


Fig. 5. Social network strategies vs. sexual partner contact tracing recruitment of people with HIV as a percentage of sampled individuals. The horizontal axis is HIV prevalence in the BSMM population. The prevalences of HIV are 36.3% (our estimate of prevalence in the BSMM population in Chicago), 27.2%, which is 75% of our estimate, 18.1%, which is 50% of our estimate, and 9.1%, which is 25% of our estimate. The percentage of PWH (panel a), OoC (panel b), and UD (undiagnosed, panel c) with regard to the number of recruited individuals decreased with decreasing prevalence, and more so for SNS versus SPCT. However, the absolute number of PWH recruited was always greater with SNS. Medians and CIs plotted here are given in Supplemental Tables S10–S12, http://links.lww.com/QAD/D23. The greater CIs in SPCT are likely due to a much smaller sample size. BSMM, Black sexual minority men; CI, confidence interval; OoC, out-of-care; PWH, people with HIV; SNS, social network strategies; SPCT, sexual partner contact tracing.

the desired alternative; if the desired outcome is a greater absolute number of undiagnosed individuals, then SNS is the preferred strategy.

Previous research has found that strategies that elicit social rather than sexual contacts are effective at identifying individuals' OoC and unaware of their HIV infection [19,20,23,39–43]. Moreover, a recent systematic study concluded that SNS is an effective way of reaching urban BSMM who are at high risk but not engaged with the healthcare system [44]. Our results corroborate these findings by providing a direct comparison between SNS and SPCT. In addition, we found that the difference in absolute numbers between PRE strategies was not because of SPCT being limited to follow-up with only PWH (see mod-SPCT in Fig. 2b), or the difference in acceptance rates between the two strategies. Rather, the differential connectivity of the two networks is likely the primary reason for the low numbers identified with SPCT; specifically, the social network is more densely connected. Because of this, we speculate that SNS is more effective at identifying preexposure prophylaxis (PrEP) candidates.

There is interest by public health officials on a national level in utilizing molecular cluster analysis with partner services to respond to emerging clusters of HIV infection. However, there is no consensus on which response methods are most effective. We found that SNS displayed a slightly higher trend in detecting indirect pairs, but neither PRE strategy was successful at identifying direct transmission pairs. Our results indicate that recovery of a significant portion of g^{gcn} remains out-of-reach without a greatly increased sample size. Diagnoses at an earlier stage of infection could increase the probability of genetic linkage and our ability to identify direct/indirect transmission pairs [45] (see also Supplemental Figure S3, http://links.lww.com/QAD/D23), as would an overall increase in viral sequence reporting completeness, which is still quite low across the country [46,47].

Our modeling study has several limitations.

(1) Our social network parameters are estimated for the BSMM population in Chicago, with study participants in the 16–29 age range; therefore, the results may not be generalizable to other communities.
(2) Our simulations assume that the recruitment probabilities among people who are newly diagnosed with HIV are the same as among people living with established HIV infection.
(3) We simulated a fixed population in which death, immigration, emigration, and entry into the young BSMM population were not modeled over the 6-year period of the simulations.
(4) The probability of recruiting an individual can be affected by compensation. The uConnect study provided compensation and was the basis of our estimate for social contact acceptance. However, the literature basis for contact tracing did not include compensation. Our sensitivity analysis with varying acceptance rates partially mitigates this limitation.
(5) Our PRE strategies are not performed simultaneously with disease spread. As these strategies could be used to contain spread, such a process could alter the epidemic. Future studies should model a combination of strategies and complex social behaviors simultaneously with disease spread to identify which package of interventions are most effective at curtailing the epidemic in specific jurisdictions.

In conclusion, the simulations presented here provided insight on the utility of different network-based recruitment strategies to attempt engagement and re-engagement in individuals with the highest transmission potential, and consequently identified which strategy has the largest impact on curtailing transmission. With no limitations on test availability, SNS was the more effective strategy for identifying undiagnosed and OoC PWH. Neither SNS nor SPCT could identify sufficient indirect or direct transmission pairs to investigate transmission networks.

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Code availability: All scripts and configuration files used to generate the results in this paper are available at https://github.com/breecummins/social_sampling_in_epidemics.git.

Conflicts of interest

There are no conflicts of interest.

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